

RAW SEQUENCE LISTING

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Application Serial Number: 10/573,135
Source: IFWP
Date Processed by STIC: 4/26/06

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IFWP

RAW SEQUENCE LISTING

DATE: 04/26/2006

PATENT APPLICATION: US/10/573,135

TIME: 07:31:36

Input Set : F:\39670a.txt

Output Set : N:\CRF4\04262006\J573135.raw

5 <110> APPLICANT: Alitalo et al
 7 <120> TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR OLIGODENDROCYTES
 9 <130> FILE REFERENCE: 28967/39670A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/573,135
 C--> 11 <141> CURRENT FILING DATE: 2006-03-23
 11 <160> NUMBER OF SEQ ID NOS: 38
 13 <170> SOFTWARE: PatentIn version 3.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 2772
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(2772)
 24 <400> SEQUENCE: 1
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 26 Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
 27 1 5 10 15
 29 gcc ccg gcc ggc gct ttt cgc aac gat gaa tgt ggc gat act ata aaa 96
 30 Ala Pro Ala Gly Ala Phe Arg Asn Asp Glu Cys Gly Asp Thr Ile Lys
 31 20 25 30
 33 att gaa agc ccc ggg tac ctt aca tct cct ggt tat cct cat tct tat 144
 34 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
 35 35 40 45
 37 cac cca agt gaa aaa tgc gaa tgg ctg att cag gct ccg gac cca tac 192
 38 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
 39 50 55 60
 41 cag aga att atg atc aac ttc aac cct cac ttc gat ttg gag gac aga 240
 42 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
 43 65 70 75 80
 45 gac tgc aag tat gac tac gtg gaa gtc ttc gat gga gaa aat gaa aat 288
 46 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
 47 85 90 95
 49 gga cat ttt agg gga aag ttc tgt gga aag ata gcc cct cct cct gtt 336
 50 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
 51 100 105 110
 53 gtg tct tca ggg cca ttt ctt ttt atc aaa ttt gtc tct gac tac gaa 384
 54 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 55 115 120 125
 57 aca cat ggt gca gga ttt tcc ata cgt tat gaa att ttc aag aga ggt 432
 58 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
 59 130 135 140
 61 cct gaa tgt tcc cag aac tac aca aca cct agt gga gtg ata aag tcc 480

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62 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
63 145                               150                               155                               160
65 ccc gga ttc cct gaa aaa tat ccc aac agc ctt gaa tgc act tat att      528
66 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
67                               165                               170                               175
69 gtc ttt gcg cca aag atg tca gag att atc ctg gaa ttt gaa agc ttt      576
70 Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
71                               180                               185                               190
73 gac ctg gag cct gac tca aat cct cca ggg ggg atg ttc tgt cgc tac      624
74 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
75                               195                               200                               205
77 gac cgg cta gaa atc tgg gat gga ttc cct gat gtt ggc cct cac att      672
78 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
79                               210                               215                               220
81 ggg cgt tac tgt gga cag aaa aca cca ggt cga atc cga tcc tca tcg      720
82 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
83 225                               230                               235                               240
85 ggc att ctc tcc atg gtt ttt tac acc gac agc gcg ata gca aaa gaa      768
86 Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
87                               245                               250                               255
89 ggt ttc tca gca aac tac agt gtc ttg cag agc agt gtc tca gaa gat      816
90 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
91                               260                               265                               270
93 ttc aaa tgt atg gaa gct ctg ggc atg gaa tca gga gaa att cat tct      864
94 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
95                               275                               280                               285
97 gac cag atc aca gct tct tcc cag tat agc acc aac tgg tct gca gag      912
98 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
99                               290                               295                               300
101 cgc tcc cgc ctg aac tac cct gag aat ggg tgg act ccc gga gag gat      960
102 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
103 305                               310                               315                               320
105 tcc tac cga gag tgg ata cag gta gac ttg ggc ctt ctg cgc ttt gtc      1008
106 Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
107                               325                               330                               335
109 acg gct gtc ggg aca cag ggc gcc att tca aaa gaa acc aag aag aaa      1056
110 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
111                               340                               345                               350
113 tat tat gtc aag act tac aag atc gac gtt agc tcc aac ggg gaa gac      1104
114 Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp
115                               355                               360                               365
117 tgg atc acc ata aaa gaa gga aac aaa cct gtt ctc ttt cag gga aac      1152
118 Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn
119                               370                               375                               380
121 acc aac ccc aca gat gtt gtg gtt gca gta ttc ccc aaa cca ctg ata      1200
122 Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile
123 385                               390                               395                               400
125 act cga ttt gtc cga atc aag cct gca act tgg gaa act ggc ata tct      1248
126 Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser

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127		405		410		415	
129	atg aga ttt gaa gta tac ggt tgc aag ata aca gat tat cct tgc tct						1296
130	Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser						
131		420		425		430	
133	gga atg ttg ggt atg gtg tct gga ctt att tct gac tcc cag atc aca						1344
134	Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr						
135		435		440		445	
137	tca tcc aac caa gga gac aga aac tgg atg cct gaa aac atc cgc ctg						1392
138	Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu						
139		450		455		460	
141	gta acc agt cgc tct ggc tgg gca ctt cca ccc gca cct cat tcc tac						1440
142	Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr						
143	465		470		475	480	
145	atc aat gag tgg ctc caa ata gac ctg ggg gag gag aag atc gtg agg						1488
146	Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg						
147		485		490		495	
149	ggc atc atc att cag ggt ggg aag cac cga gag aac aag gtg ttc atg						1536
150	Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met						
151		500		505		510	
153	agg aag ttc aag atc ggg tac agc aac aac ggc tcg gac tgg aag atg						1584
154	Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met						
155		515		520		525	
157	atc atg gat gac agc aaa cgc aag gcg aag tct ttt gag ggc aac aac						1632
158	Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn						
159		530		535		540	
161	aac tat gat aca cct gag ctg cgg act ttt cca gct ctc tcc acg cga						1680
162	Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg						
163	545		550		555	560	
165	ttc atc agg atc tac ccc gag aga gcc act cat ggc gga ctg ggg ctc						1728
166	Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu						
167		565		570		575	
169	aga atg gag ctg ctg ggc tgt gaa gtg gaa gcc cct aca gct gga ccg						1776
170	Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro						
171		580		585		590	
173	acc act ccc aac ggg aac ttg gtg gat gaa tgt gat gac gac cag gcc						1824
174	Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala						
175		595		600		605	
177	aac tgc cac agt gga aca ggt gat gac ttc cag ctc aca ggt ggc acc						1872
178	Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr						
179		610		615		620	
181	act gtg ctg gcc aca gaa aag ccc acg gtc ata gac agc acc ata caa						1920
182	Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln						
183	625		630		635	640	
185	tca gag ttt cca aca tat ggt ttt aac tgt gaa ttt ggc tgg ggc tct						1968
186	Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser						
187		645		650		655	
189	cac aag acc ttc tgc cac tgg gaa cat gac aat cac gtg cag ctc aag						2016
190	His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys						
191		660		665		670	

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193 tgg agt gtg ttg acc agc aag acg gga ccc att cag gat cac aca gga      2064
194 Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly
195      675      680      685
197 gat ggc aac ttc atc tat tcc caa gct gac gaa aat cag aag ggc aaa      2112
198 Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
199      690      695      700
201 gtg gct cgc ctg gtg agc cct gtg gtt tat tcc cag aac tct gcc cac      2160
202 Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His
203 705      710      715      720
205 tgc atg acc ttc tgg tat cac atg tct ggg tcc cac gtc ggc aca ctc      2208
206 Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu
207      725      730      735
209 agg gtc aaa ctg cgc tac cag aag cca gag gag tac gat cag ctg gtc      2256
210 Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val
211      740      745      750
213 tgg atg gcc att gga cac caa ggt gac cac tgg aag gaa ggg cgt gtc      2304
214 Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val
215      755      760      765
217 ttg ctc cac aag tct ctg aaa ctt tat cag gtg att ttc gag ggc gaa      2352
218 Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu
219      770      775      780
221 atc gga aaa gga aac ctt ggt ggg att gct gtg gat gac att agt att      2400
222 Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
223 785      790      795      800
225 aat aac cac att tca caa gaa gat tgt gca aaa cca gca gac ctg gat      2448
226 Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp
227      805      810      815
229 aaa aag aac cca gaa att aaa att gat gaa aca ggg agc acg cca gga      2496
230 Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
231      820      825      830
233 tac gaa ggt gaa gga gaa ggt gac aag aac atc tcc agg aag cca ggc      2544
234 Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
235      835      840      845
237 aat gtg ttg aag acc tta gaa ccc atc ctc atc acc atc ata gcc atg      2592
238 Asn Val Leu Lys Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile Ala Met
239      850      855      860
241 agc gcc ctg ggg gtc ctc ctg ggg gct gtc tgt ggg gtc gtg ctg tac      2640
242 Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr
243 865      870      875      880
245 tgt gcc tgt tgg cat aat ggg atg tca gaa aga aac ttg tct gcc ctg      2688
246 Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu
247      885      890      895
249 gag aac tat aac ttt gaa ctt gtg gat ggt gtg aag ttg aaa aaa gac      2736
250 Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp
251      900      905      910
253 aaa ctg aat aca cag agt act tat tgc gag gca tga      2772
254 Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala
255      915      920
258 <210> SEQ ID NO: 2

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259 <211> LENGTH: 923

260 <212> TYPE: PRT

261 <213> ORGANISM: Homo sapiens

263 <400> SEQUENCE: 2

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269 Ala Pro Ala Gly Ala Phe Arg Asn Asp Glu Cys Gly Asp Thr Ile Lys
270          20          25          30
273 Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
274          35          40          45
277 His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
278          50          55          60
281 Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
282 65          70          75          80
285 Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
286          85          90          95
289 Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val
290          100         105         110
293 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
294          115         120         125
297 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
298          130         135         140
301 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
302 145         150         155         160
305 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
306          165         170         175
310 Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
311          180         185         190
314 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
315          195         200         205
319 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
320          210         215         220
323 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
324 225         230         235         240
327 Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
328          245         250         255
331 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
332          260         265         270
335 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
336          275         280         285
339 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
340          290         295         300
343 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
344 305         310         315         320
347 Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
348          325         330         335
351 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
352          340         345         350
355 Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date